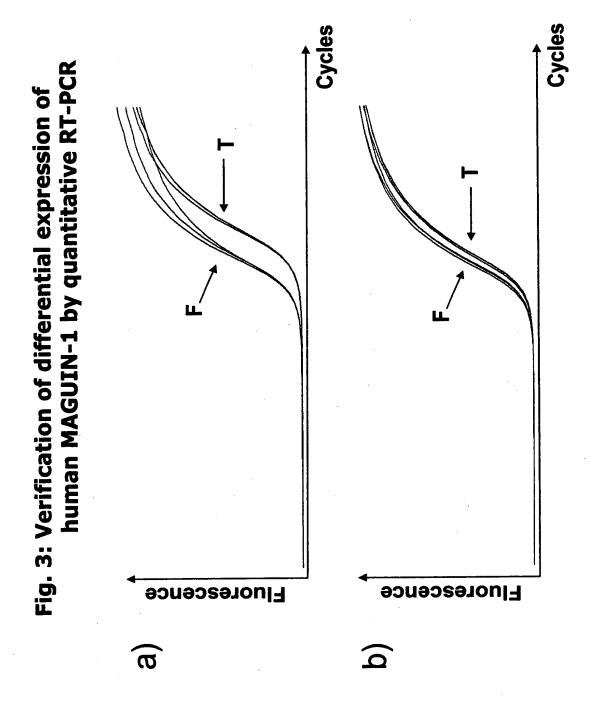
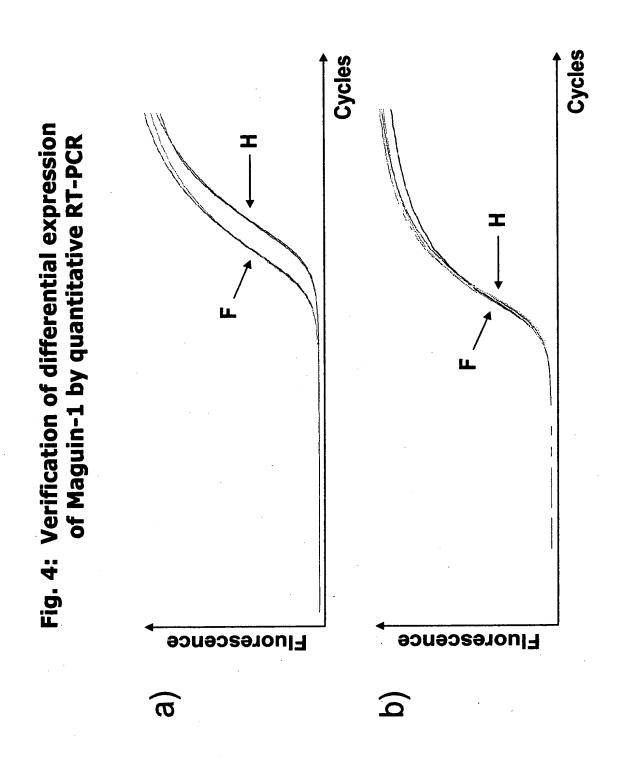
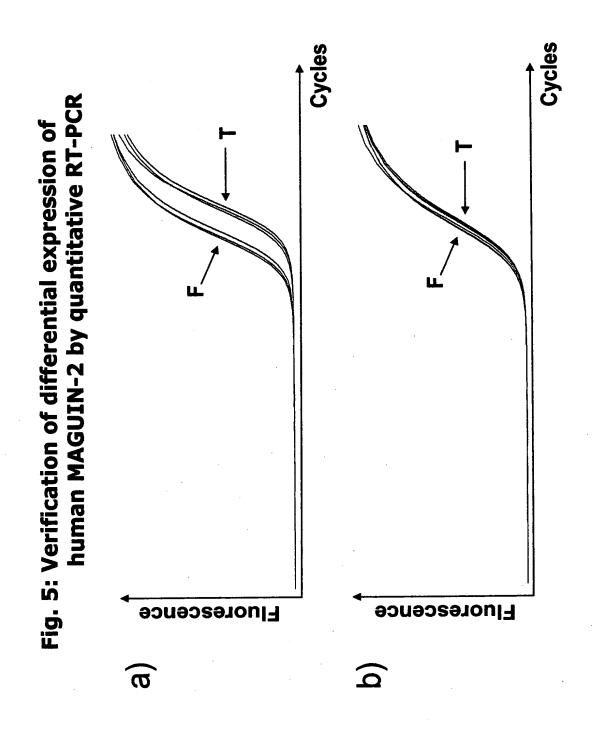


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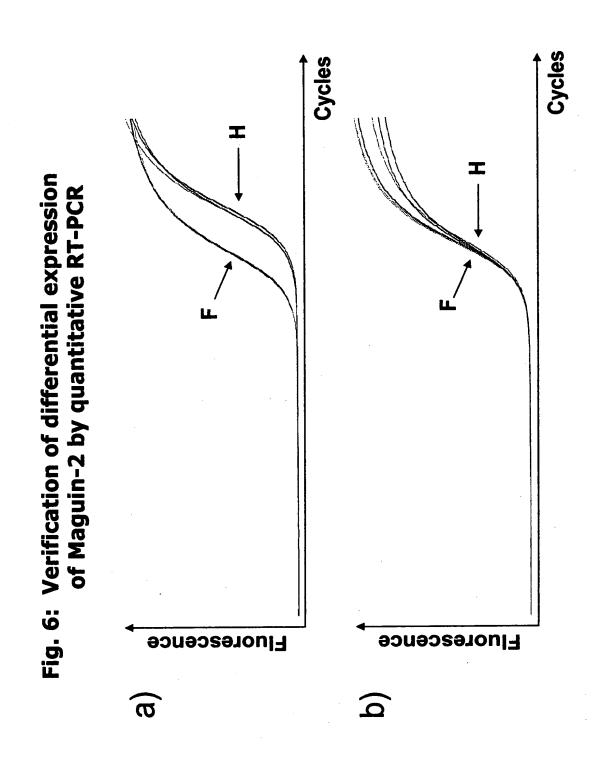
f:;







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Fig. 7: SEQ ID NO. 1: amino acid sequence of human MAGUIN-1 protein

Length: 1034 aa

1	MALIMEPVSK WSPSQVVDWM KGLDDCLQQY IKNFEREKIS GDQLLRITHQ
51	ELEDLGVSRI GHQELILEAV DLLCALNYGL ETENLKTLSH KLNASAKNLQ
101	NFITGRRRSG HYDGRTSRKL PNDFLTSVVD LIGAAKSLLA WLDRSPFAAV
151	TDYSVTRNNV IQLCLELTTI VQQDCTVYET ENKILHVCKT LSGVCDHIIS
201	LSSDPLVSQS AHLEVIQLAN IKPSEGLGMY IKSTYDGLHV ITGTTENSPA
251	DRCKKIHAGD EVIQVNHQTV VGWQLKNLVN ALREDPSGVI LTLKKRPQSM
301	LTSAPALLKN MRWKPLALQP LIPRSPTSSV ATPSSTISTP TKRDSSALQD
351	LYIPPPPAEP YIPRDEKGNL PCEDLRGHMV GKPVHKGSES PNSFLDQEYR
401	KRFNIVEEDT VLYCYEYEKG RSSSQGRRES TPTYGKLRPI SMPVEYNWVG
451	DYEDPNKMKR DSRRENSLLR YMSNEKIAQE EYMFQRNSKK DTGKKSKKKG
501	DKSNSPTHYS LLPSLQMDAL RQDIMGTPVP ETTLYHTFQQ SSLQHKSKKK
551	NKGPIAGKSK RRISCKDLGR GDCEGWLWKK KDAKSYFSQK WKKYWFVLKI
601	ASLYWYINEE DEKAEGFISL PEFKIDRASE CRKKYAFKAC HPKIKSFYFA
651	AEHLDDMNRW LNRINMLTAG YAERERIKQE QDYWSESDKE EADTPSTPKQ
701	DSPPPPYDTY PRPPSMSCAS PYVEAKHSRL SSTETSQSQS SHEEFRQEVT
751	GSSAVSPIRK TASQRRSWQD LIETPLTSSG LHYLQTLPLE DSVFSDSAAI
801	SPEHRRQSTL PTQKCHLQDH YGPYPLAESE RMQVLNGNGG KPRSFTLPRD
851	SGFNHCCLNA PVSACDPQDD VQPPEVEEEE EEEEEEGEAA GENIGEKSES
901	REEKLGDSLQ DLYRALEQAS LSPLGEHRIS TKMEYKLSFI KRCNDPVMNE
951	KLHRLRILKS TLKAREGEVA IIDKVLDNPD LTSKEFQQWK QMYLDLFLDI
1001	CQNTTSNDPL SISSEVDVIT SSLAHTHSYI ETHV*

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Fig. 8: Alignment of SEQ ID NO. 1, human MAGUIN-1, with rat MAGUIN-1

Length: 1034 aa

1	MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ	50
1	MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ	50
51	ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ	100
51	ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ	100
101	NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV	150
101	NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV	150
151	TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS	200
151	TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS	200
201	LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA	250
201	LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA	250
251	DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM	300
251	DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM	300
301	LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD	350
301	LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD	350
351	LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR	400
351		400
401	KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG	450
401		450
451	DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKG	500
451	DAED DIAMAND DEBENGT I DAMENER I VOLEAMEO DIZKRULCHK ZRRRC	500

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501	DKSNSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK	550
501	DKSTSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK	550
551	NKGPIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD	600
551	NKGAIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD	600
601	ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA	650
601	ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA	650
651	AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ	700
651	AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ	700
701	DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT	750
701	DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT	750
751	GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI	800
751	GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI	800
801	SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD	850
801	SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD	850
851	SGFNHCCLNAPVSACDPQDDVQPPEVEEEEEEEEEEEAAGENIGEKSES	900
	SGFNHCCLNAPVSACDPQDDIQPPEVEEEEEEEEEEAAGENIGEKNEN	898
901	REEKLGDSLQDLYRALEQASLSPLGEHRISTKMEYKLSFIKRCNDPVMNE	950
899	REEKLGDSLQDLYRALEEASLSPLGEHRISTKIEYKLSFIKRCNDPVMNE	948
	KLHRLRILKSTLKAREGEVAIIDKVLDNPDLTSKEFQQWKQMYLDLFLDI	1000
	KLHRLRILKSTLKAREGEVAIIDKVLDNPDLTSKEFQQWKQMYLDLFLDI	998
	CQNTTSNDPLSISSEVDVITSSLAHTHSYIETHV 1034	
999	CQNTTSNDPLSISSEVDVITSSLTHTHSYIETHV 1032	

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Fig. 9: SEQ ID NO. 2: amino acid sequence of human MAGUIN-2 protein

Length: 898 aa

1 MALIMEPVSK WSPSQVVDWM KGLDDCLQQY IKNFEREK

- 51 ELEDLGVSRI GHQELILEAV DLLCALNYGL ETENLKTLSH KLNASAKNLQ
- 101 NFITGRRRSG HYDGRTSRKL PNDFLTSVVD LIGAAKSLLA WLDRSPFAAV
- 151 TDYSVTRNNV IQLCLELTTI VQQDCTVYET ENKILHVCKT LSGVCDHIIS
- 201 LSSDPLVSQS AHLEVIQLAN IKPSEGLGMY IKSTYDGLHV ITGTTENSPA
- 251 DRCKKIHAGD EVIQVNHQTV VGWQLKNLVN ALREDPSGVI LTLKKRPQSM
- 301 LTSAPALLKN MRWKPLALQP LIPRSPTSSV ATPSSTISTP TKRDSSALQD
- 351 LYIPPPPAEP YIPRDEKGNL PCEDLRGHMV GKPVHKGSES PNSFLDQEYR
- 401 KRFNIVEEDT VLYCYEYEKG RSSSQGRRES TPTYGKLRPI SMPVEYNWVG
- 451 DYEDPNKMKR DSRRENSLLR YMSNEKIAQE EYMFQRNSKK DTGKKSKKKG
- 501 DKSNSPTHYS LLPSLQMDAL RQDIMGTPVP ETTLYHTFQQ SSLQHKSKKK
- 551 NKGPIAGKSK RRISCKDLGR GDCEGWLWKK KDAKSYFSQK WKKYWFVLKD
- 601 ASLYWYINEE DEKAEGFISL PEFKIDRASE CRKKYAFKAC HPKIKSFYFA
- 651 AEHLDDMNRW LNRINMLTAG YAERERIKQE QDYWSESDKE EADTPSTPKQ
- 701 DSPPPPYDTY PRPPSMSCAS PYVEAKHSRL SSTETSQSQS SHEEFRQEVT
- 751 GSSAVSPIRK TASQRRSWQD LIETPLTSSG LHYLQTLPLE DSVFSDSAAI
- 801 SPEHRROSTL PTOKCHLODH YGPYPLAESE RMQVLNGNGG KPRSFTLPRD
- 851 SGFNHCCLNA PVSACDPQDD VQPPEVEEEE EEEEEEGEAA GENIGEKS*

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Figure 10: Alignment of SEQ ID NO. 2, human MAGUIN-2, with rat MAGUIN-2

Length: 898 aa

	MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ	50 50
51		100
51		100
101		150
101	NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV	150
151	TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS	200
151	TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS	200
201	LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA	250
201	LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA	250
251251	DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM	300
301	LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD	350
301		350
351	LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR	400
351	LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR	400
401	KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG	450
401	KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG	450
451		500
451	DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKG	500

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501	DKSNSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK	550
501	DKSTSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK	550
551		600
551	NKGAIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD	600
601		650
601	ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA	650
651	AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ	700
651	AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ	700
701	DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT	750
701	DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT	750
751	GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI	800
751	GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI	800
801	SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD	850
801	SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD	850
851	SGFNHCCLNAPVSACDPQDDVQPPEVEEEEEEEEEEGEAAGENIGEKS	98
851	SGFNHCCLNAPVSACDPQDDIQPPEVEEEEEEEEEEAAGENIGEKS	96

-13/26-Fig. 11: SEQ ID NO. 3: nucleotide sequence of human MAGUIN-1 coding sequence

Length: 3105 bp

	_					
1	ATGGCTCTGA	TAATGGAACC	GGTGAGCAAA	TGGTCTCCGA	GTCAAGTAGT	GGACTGGATG
61	AAAGGTCTTG	ATGACTGTTT	GCAGCAGTAT	ATTAAGAACT	TTGAGAGGGA	GAAGATCAGT
121	GGGGACCAGC	TGCTGCGCAT	TACACATCAG	GAGCTAGAAG	ATCTGGGGGT	CAGCCGCATT
181	GGCCATCAGG	AACTGATCTT	GGAAGCAGTT	GACCTTCTGT	GTGCATTGAA	TTATGGCTTG
241	GAAACAGAAA	ATCTAAAAAC	CCTTTCTCAC	AAGTTGAATG	CATCTGCCAA	AAATCTGCAG
301	AATTTTATAA	CAGGAAGGAG	AAGGAGTGGC	CATTATGATG	GGAGGACCAG	CCGAAAATTG
361	CCAAACGACT	TTCTGACCTC	AGTTGTGGAT	CTGATTGGAG	CAGCCAAGAG	TCTGCTTGCC
421	TGGTTGGACA	GGTCACCATT	TGCTGCTGTG	ACAGACTATT	CAGTTACAAG	AAATAATGTC
481	ATACAACTCT	GCCTGGAGTT	AACAACAATT	GTGCAACAGG	ATTGTACTGT	ATATGAAACA
541	GAGAATAAAA	TTCTTCACGT	GTGTAAAACT	CTTTCTGGAG	TCTGTGACCA	CATCATATCC
601	CTGTCGTCAG	ATCCTCTGGT	TTCACAGTCT	GCTCACCTGG	AAGTGATTCA	ACTGGCAAAC
661	ATTAAACCAA	GCGAAGGGCT	GGGTATGTAT	ATTAAATCTA	CATATGATGG	CCTCCATGTA
721	ATTACTGGAA	CCACAGAAAA	TTCACCTGCA	GATCGGTGCA	AGAAAATCCA	TGCTGGCGAT
			TCAGACTGTG			
841	GCACTACGAG	AGGACCCGAG	TGGTGTTATC	TTAACTTTGA	AAAAGCGACC	TCAGAGCATG
901	CTTACCTCAG	CACCAGCTTT	ACTGAAAAAT	ATGAGATGGA	AGCCCCTTGC	TCTGCAGCCT
961	CTTATACCTA	GAAGTCCCAC	AAGCAGCGTT	GCCACGCCTT	CCAGCACCAT	CAGTACACCC
1021	ACCAAAAGAG	ACAGTTCTGC	CCTCCAGGAT	CTCTACATTC	CCCCTCCTCC	TGCAGAACCA
1081	TATATTCCCA	GGGATGAAAA	AGGAAACCTT	CCTTGTGAAG	ACCTCAGAGG	ACATATGGTG
1141	GGCAAGCCAG	TGCATAAGGG	ATCTGAATCA	CCAAATTCAT	TTCTGGATCA	GGAATATCGA
1201	AAGAGATTTA	ATATTGTCGA	AGAAGATACT	GTCTTATATT	GCTATGAATA	TGAAAAAGGA
1261	AGATCAAGTA	GTCAAGGAAG	ACGAGAAAGC	ACCCCAACTT	ATGGCAAGCT	ACGACCTATA
1321	TCTATGCCAG	TGGAATATAA	TTGGGTGGGG	GACTATGAAG	ATCCAAATAA	GATGAAGAGA
1381			TCTACTTCGG			
1441	GAATACATGT	TTCAGAGAAA	CAGCAAAAAG	GACACAGGGA	AGAAGTCAAA	AAAGAAGGGT
			TCACTATTCA			
1561	AGACAAGACA	TCATGGGCAC	TCCTGTGCCA	GAGACCACAC	TATACCATAC	ATTTCAGCAG
1621	TCCTCACTGC	AGCACAAATC	AAAGAAGAAA	AACAAAGGTC	CTATAGCAGG	CAAGAGCAAA
1681	AGACGAATTT	CTTGCAAAGA	TCTTGGCCGT	GGTGACTGTG	AGGGCTGGCT	TTGGAAAAAG
1741	AAAGATGCGA	AGAGTTACTT	TTCACAGAAA	TGGAAAAAAT	ATTGGTTTGT	CCTAAAGGAT
1801	GCATCCCTTT	ATTGGTATAT	TAATGAGGAG	GATGAAAAAG	CAGAAGGATT	CATTAGCCTG
1861	CCTGAATTTA	AAATTGATAG	AGCCAGTGAA	TGCCGCAAAA	AATATGCATT	CAAAGCCTGT
1921	CATCCTAAAA	TCAAAAGCTT	TTATTTTGCT	GCTGAACATC	TTGATGATAT	GAACAGGTGG
			GACTGCAGGA			
2041	CAAGATTACT	GGAGTGAGAG	TGACAAGGAA	GAAGCAGATA	CTCCATCAAC	ACCAAAACAA
			TGATACATAC			
			TAGCCGACTT			
			GGAAGTAACT			
			CTGGCAGGAT			
			GCCCCTGGAG			
			GTCTACCCTG			
			TGAGAGTGAG			
			GCCTCGAGAT			
			ACAGGATGAC			
			GGAGGCAGCA			
			CTCATTGCAA			
			TCGTATTTCA			
			AATGAATGAA			
			GGAAGTAGCC			
			ACAATGGAAG			
			TGACCCACTG			
			TTCATACATT			

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Fig. 12: SEQ ID NO. 4: nucleotide sequence of human MAGUIN-2 coding sequence

Length: 2697 bp

1 ATGGCTCTGA TAAAGGACC GGTGAGGAG ATGGATGTTT GCAGCAGTAT ATTAAGAACT 101 TTGAGAGGAG AAAGGTCTTG ATGACGTTT GCAGCAGCT TACACATCAG 151 GAGCTAGAGA ATCTGAGAGA ACTGATCTT GGGGACCAGC TGCTGCGCAT TACACACCAG 251 AATTTATAA CAGCGAGAT GGCCATTGAG AAACAGCAAA 301 AATTTATAA CAGGAGAGT TTCTGACCC CATTATGAG GGAGACACT 401 CAGCCAAGAG TCTGCTTGCC TGGTTGACAC GGTCACACAT TGCTGCTGTG 501 AACAACAAT GTCCACACAGG ATTAACACA GGTAGACATT GCCTGAACTT 651 TCTTCTGCTAG ATCTCTGGT TTCACAGTCT GCTCACCTGG AAGAAAAAACA GAGAGGACT 651 GCTGGAACA ATTAACACAA GCTCAAGTATT ATTACTGAACAG ATTAACACAA GCTCACCTGG GCTCACCTGG ATTAACACAA AGATAGATAA ATTACTGAACACA ATTAACACAA AGATATATCA AGCTGATGAGA ACTAATAGAGA ACTAATACAGA ACTAATAGAGA ACTAATAGAGA ACTAATAGAGA ACTAAT						
GGACTGGATG AAAGGTCTTG ATGACTGTTT GCACCAGTAT ATTAAGAACT	1	ATGGCTCTGA	TAATGGAACC	GGTGAGCAAA	TGGTCTCCGA	GTCAAGTAGT
151 GAGCTAGARA ATCTGGGGGT CAGCCGCATT GGCATCAGG AACTGACTAGA AACTGACATT GACACCAGT GACACCAGT GACACCAGT GACACCAGA AAATCTGCAA AAATCTGCAA AAATCTGCAA AAATCTGCAA AAATCTGCAA AAATCTGCCAA AAATCTGCAA AAATCTGCCAA AATCTGCCAA AAATCTGCCAA GGGAGCCAG CATTGGCTAGC CAGTGGGGACAAC CATTGGCTAGC CAGTGGGGACAAC CATTGGCTAGC CAGTGGGACAAC CATTGGCTAGA AATTATGACACA GGCTGGCAATC CAGCACAGAT TTCTTCACGT GTGTAAAACT CTTTCTGCAGT GTGTACACTGG AACTCATATCA CGCTGGCAAAC ATTCAAACCAA CTTTCTGGAG CCTTCACTGTA AATTATCAACTGT ATTATGACAAC ACCACAGAAAA ATTAAACCAA GCGAGGGGC GGGTAGCAAAC ATTAAACCAA GCGAGGGGGC AGGTAGTATCA ACCACAGAAAA ATTAAACCAA AGTTAATCA ACCACAGAAAA ATTAAACCAA AGTTAAACAA ATTAAACCAA AGTTAAACAA ATTAAACCAA AGTTGAGAACA ATTAAACCAA AGTTGAGAACAA TTAAACTTAA ACACAGAAAAA ATTAAACCAA AGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		GGACTGGATG	AAAGGTCTTG	ATGACTGTTT	GCAGCAGTAT	ATTAAGAACT
151 GAGCTAGARA ATCTGGGGGT CAGCCGCATT GGCATCAGG AACTGACTAGA AACTGACATT GACACCAGT GACACCAGT GACACCAGT GACACCAGA AAATCTGCAA AAATCTGCAA AAATCTGCAA AAATCTGCAA AAATCTGCAA AAATCTGCCAA AAATCTGCAA AAATCTGCCAA AATCTGCCAA AAATCTGCCAA GGGAGCCAG CATTGGCTAGC CAGTGGGGACAAC CATTGGCTAGC CAGTGGGGACAAC CATTGGCTAGC CAGTGGGACAAC CATTGGCTAGA AATTATGACACA GGCTGGCAATC CAGCACAGAT TTCTTCACGT GTGTAAAACT CTTTCTGCAGT GTGTACACTGG AACTCATATCA CGCTGGCAAAC ATTCAAACCAA CTTTCTGGAG CCTTCACTGTA AATTATCAACTGT ATTATGACAAC ACCACAGAAAA ATTAAACCAA GCGAGGGGC GGGTAGCAAAC ATTAAACCAA GCGAGGGGGC AGGTAGTATCA ACCACAGAAAA ATTAAACCAA AGTTAATCA ACCACAGAAAA ATTAAACCAA AGTTAAACAA ATTAAACCAA AGTTAAACAA ATTAAACCAA AGTTGAGAACA ATTAAACCAA AGTTGAGAACAA TTAAACTTAA ACACAGAAAAA ATTAAACCAA AGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	101	TTGAGAGGGA	GAAGATCAGT	GGGGACCAGC	TGCTGCGCAT	TACACATCAG
ANTITATAMA CAGGANGGA AAGTAGATG CATTATGATA GAGAGACCAG 301 AATTTTAMA CAGGANGGAG AAGGAGTGGC CATTATGATG GGAGACCAG 351 CCGAAAATTG CCAAACGACT TTCTGACCTC AGTTGATGATG GGAGACCAG 401 CAGCCAAGAG TCTGCTTGCC TGGTTGGACA GGTCACCATT TGCTGCTGTG 401 CAGCCAAGAG TCTGCTTGCC TGGTTGGACA GGTCACCATT TGCTGCTGTG 501 AACAACAATT CAGTTACAAG AAATAATGCTC ATACAACCTC GCCTGGGGTT 501 AACAACAATT GTGCAACAGG ATTGTACAGT ATACAACTCT GCCTGGGGTT 601 CTGTCGTCAG ATCCTCTGGT TTCACGAGT TGCTCACCTGG AAGTGATACA 601 CTGTCGTCAG ATCCTCTGGT TTCACGAGTCT GCCTGGAGTT 601 CTGTCGTCAG ATCCTCTGGT TTCACGAGTCT GCCTGCACCTG AAGTGATTCA 601 CTGTCGTCAG ATCCTCTGGT TTCACGAGTCT GCTCACCTGC AAGTGATTCA 601 CATATGATGG CCTCCATGTA ATACTGGAA CCCACGAAAAA TTCACCTGCA 701 CATATGATGG CCTCCATGTA ATACTGGAA CCCACGAAAAA TTCACCTGCA 701 CATATGATGG GTGGGGTGCC AGTTGAAAAA TTTGGTGAAT ATTACACTGCA 801 TCAGACCCAG TGGGGTTGAC AGTACAAAAAA ATTACACTGCA 801 TCAGACCCAG TGGTGTTATAC TTAACTTTGA AAAAGCGACC TCAGGAGCATG 901 CTTACCTCAG CACCACCATTA ACTGAAAAAA ATGAGAAGCA CTCAGGACAT 901 CTTACCTCAG CACCACCACAAAAGAG ACAGTTCTCAC 901 CTCACACACC CACAAAAGAG ACAGTTCTCC CCTCCAGGAT 1001 CCAGGACCCAT CAGTACCCC ACCAAAAGAG ACAGTTCTCC CCTCCAGGAT 1001 CCAGGACCAT CAGTACACCC ACCAAAAGAG ACAGTTCTCC CCTCCAGGAT 1001 CCAGGACCAT CAGTACACC ACCAAAAGAG ACAGTTCTCAC GCCACGCCTT 1001 CCAGGACCAT CAGTACACC ACCAAAAGAG ACAGTTCTCC CCTCCAGGAT 1001 AAGAGATTA ATATTGTGAA ACCTCAAAGAG ACAGTTCTCC CCTCCAGGAT 1001 AAGAGATTA ATATTGTGAA AGAGAATACT TTCTGGATCA GGAAAACTC 1001 AAGAGATTA ATATTGTGAA AGAGAATACT TTCTGGATCA GGAAAACTC 1001 AAGAGATTA ATATTGTGAA AGAGAAAACT TTCTATATT GCTAAAAAA 1101 AGAGAACCT CCTCAAATAA GATGAAAGAG ACGACAAAAA AAAACAACA CCCCAAATTA 1101 ATGCCAAGC AGACAAAAAA GACACAAAAAAAAAAAAA	151					
351 CCGAAAATTG CCAAACGAC TTCTGACCTC AGTTGTGAT CTGATTGGAG 351 CCGAAAATTG CCAAACGAC TTCTGACCTC AGTTGTGAT CTGATTGGAG 451 ACAGACTATT CAGTTACAAG AATTATGTC AGTTGTGACT TGCTGCTGTG 451 ACAGACTATT CAGTTACAAG AAATAATGTC ATACAACTCT GCCTGGAGTT 501 AACAACAATT GTGCAACAGA ATTATCTC ATACAACTCT GCCTGGAGTT 501 TTCTTCACGT GTGTAAAACT CTTTCTGGAG TCTGTGACCA CATCATATCC 651 GCTGGCAAAC ATTAAAACCA GCGAAGGGCT GCTCACCTGG AAGTGATCA 651 GCTGGCAACA CATTAAAACCA GCGAAGGGCT GGGATATAATCA 701 CATATGATGG CCTCCATGTA ATTACCAGTCT GCTCACCTGG AAGTGATCA 701 CATATGATGG CCTCCATGTA ATTACCAGTCT GCTCACCTGG AAGTGATCA 701 CATATGATGG CCTCCATGTA ATTACCAGTCT GCTCACCTGG AAGTGATCA 701 CATATGATGG GGGGGGGC AGTTGAAAAA TTTCACCAGTC 701 CATACCTCCA CACCAGCTTT ATTACAAATCCA 801 TCAGACCTGTG GTGGGGGGC AGTTGAAAAA TTTGGTGAAA GCCCCTTGC 801 CTGCCACCAC CACCAGCTTT ACTAAAAATA ATTGAGGAAA GCCCCTTGC 901 CTTACCTCCAG CACCAGCTTT ACTAAAAATA ATTGAGGAAC TCAGAGCATG 901 CTTACCTCAG CACCAGCTTT ACTAAAAAATA ATTGAGGAAC TCACGAGCATG 1051 CTCTACATCC CCCCCTCCC TGCAGAACCA TATATTCCC GGGATGAAAA 1010 AGGAAACCTT CCTTGTGAAG ACCTCAGAGGA ACAGTTCTGC CCCCCCGTCT 1001 CCAGCACCAT CAGTACACC ACCAAAATCAG ACAGTTCTG CCCCCCCGTG 1151 TGCATAAGGG ATCTGAAATCA CCAAAATCAT TTCTGGATCA GGAATACGA 1151 TGCATAAGGG ATCTGAAATCA CCAAAATCAT TTCTGGATCA GGAATACGA 1151 TGCATAAGGA AGATCAAATA ATTGAGAAAAA TTCGAACCAC TATATGGAGA 1151 TGCATAAGGA AGAACAAATA ATTGAGAAAAA TTCGAACCAC TATATGAGTA ACAGAGATATA ATTTGAAATA ATTGAGAAAAAA TTCGAACCAC TATATGAGAAAAA TTCGAACCAC TATATGAACAAAAAAAAAA	201	GGAAGCAGTT	GACCTTCTGT	GTGCATTGAA	TTATGGCTTG	GAAACAGAAA
CCGAAAATTG CCAAACGACT TTCTGACTC AGTTGTGGAT CTGATTGGAG 401 CAGCCAAGAGA TCTGCTTGCC TGGTTGGACA GGTCACCATT TGCTGCTGTG 451 ACAGACTATT CAGTTACAAG AAATAATGTC ATACAACTCT GCCTGGAGTT 501 AACAACAATT GTGCAACAGG ATTGTACTAG TACAACTCT GCCTGGAGTT 501 AACAACAATT GTGCAACAGG ATTGTACTAG TTCTGGAGC CATCATATCC 601 CTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTGACCA CATCATATCC 601 CTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTGACCA CATCATATCC 601 CATATGATGG CCTCCATGTA ATACTGGAAC CATCATATCC 601 CATATGATGG CCTCCATGTA ATACTGGAA CACAGAAAA TTCACCTGCA 601 TCAGACCTGG GTGGGGTGCC AGTTGAAAAAT TTACACTGCA 601 TCAGACCGAG TGGTGTTAC TTAACTGGAA CACAGAAAA TTCACCTGCA 601 TCAGACCGAG TGGTGTTAC TTAACTGGAA CACAGAAAA TTCACCTGCA 601 TCAGACCCGA CACCAGCTTT ACTGAAAAAT ATGAGATGGA CACAGACGAG 601 TCTTACCTCAG CACCAGCTTT ACTGTAAAAAT ATGAGATGGA AGCCCCTTGC 601 CTTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA ACCCCCTTGC 601 CTTACCTCAG CACCAGCTTA CACTAACACGA CACGACACGA	251	ATCTAAAAAC	CCTTTCTCAC	AAGTTGAATG	CATCTGCCAA	AAATCTGCAG
401 CAGCCAAGAG TCTGCTTGCC TGGTTGGACA GGTCACCATT TGCTGCTGTG 451 ACAGACTATT CAGTTACAAG AATTATTC ATACAACTCT GCCTGGAGTT 501 AACAACAATT GTGCAACAGG ATTGTTACTGT ATACGAACTCT GCCTGGAGTT 501 TCTTCACGT GTGTAAAACT CTTTCTGGAG TCTGTGACCA CATCATATCC 601 CTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTCACCTGG AAGTGATTCA 601 CCTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTCACCTGG AAGTGATTCA 601 CATATGATGG CTCCATGTA ATTACTGAACA GGGAAGGCTT GGGTATGATTA 701 CATATGATGG CCTCCATGTA ATTACTGAAC AGGAAGGCT GGGTATGATTA ATTAAACCAA 801 TCAGACCTGTG GTGGGGTGC AGTTGAAAAA TTTGGTGACA GCACACGAG 801 CTGACCCAG TGGTGTTACC TACTGAAAAA TTTGGTGACA GCACACGAG 801 CTGCCACCAC CACCAGCTTT ACTGAAAAAT ATTGAGAGGCC TCAGAGCATG 901 CTTCCCTCAG CACCAGCTTT ACTGAAAAAT ATTGAGACTGG GCCCCTGG 901 CTTCACATC CCCCCCCCC TGCAGAACAC AAGCAGCGT GCCACCGCTT 1001 CCACCACCAT CAGTACACC ACCAAAACAG ACAGTTCTCC CCTCCAGGAT 1001 CTGCACACCT CCTCTCTCTC TGCAGAACCA TATATCCCA GGGATGAAC 1001 CAGCACCAT CCTTGTGAAG ACCTCAGAGG ACAGTTCCCA GGGATGAAC 1101 AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACAATTCCCA GGGATGAAC 1101 AGGAAACTT ATTGTCGA AGAAGACCA TATAGTT GCCACAGCCTT 1301 AAGCAAAATA ATATTGTCGA AGAAGACCA TATAGTT GCCACAGCCTT 1301 AAGGAAACTT ACTGAAAACA TCTCAGAGG ACAATTCCCA GGGATAATCGA 1201 AAGGAAACTT ACTGTGAAGA ACACCTAAATCA TCTCTGAAGAG ACACCACACTT 1301 ATGCCAAACA AGACCACTATA TCTATGCCAG TGCAAGCCAG 1351 GACTATGAAG ACCCCAAATCA GTCAAATCA TCTCTAAATA TGTGGGAG 1351 GACTATGAAG ACCCCAAAACA AGAAGAAC ACCCCAACTT 1401 TCTCACTTCGG TATATGACCA ATGAAAAAGAT TGCTCAAGAA AGAAAACG ACCCCAAACT 1401 TCTCACTTCGG TATATGACCA ATGAAAAAGAT TGCTCAAGAA AGAAAAAGAT TCTCAAGAGA ACCCCAAACT 1501 GATAAAAAGAA CAGCCAAAAA GAGAAAAAA ATGAAAAAAA ATGAAAAAAAA ATGAAAAAAAA	301	AATTTTATAA	CAGGAAGGAG	AAGGAGTGGC	CATTATGATG	GGAGGACCAG
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551 ACARCARTT GTGCAACAGG ATTGTACTGT ATATGAACACA GAGARTAAAA 551 TTCTTCACGT GTGTAAAACT CTTTCTGGAG TCTGTGACCA CATCATATCC 601 CTGTGGTCAG ATCCTCTGGT TTCACAGTCT GCTCACCTGG AAGTGATTCA 651 GCTGGCAAC ATTAAACCAA GCGAAGGGCT GGGTATGTA ATTAAACTAA 701 CATATGATGG CCTCCATTATA ATTACTGGAA CACAGAAAA TTCACCTGCA 751 GATCGGTGGCA AGAAAATCCA TGCTGGCGGTA GAGAGTATTC AGTTAAACCAA 801 TCAGACTGTG GTGGGGTGC AGTTAAAAAA TTTGGTGAAT GAGAGTATTCA 801 TCAGACCGAG TGGTGTTATC TTAACTTTGA AAAAGCGAC TCAGAGAGAG 851 AGGACCCGAG TGGTGTTATC TTAACTTTGA AAAAGCGAC TCAGAGACAT 901 CTTACCTCAG CACCAGCTTT ACTGAAAAAA TTTGGTGGAT GCACCACGAG 951 TCTGCAGCCT CTTATACCTA GAGTCCCC ACCAGAAGAG CCAGTTCGC 951 TCTGCAGCCT CATTACCCCA CACAAAAGAG ACAGTTCTGC CCTCCCAGGAT 1001 CCAGCACCAT CACTACACCC ACCAAAAGAG ACAGTTCTGC CCTCCCAGGAT 1001 CCAGCACCAT CCTTGTGAAG ACCTCAGAG ACATTATGTCCA GGATGAAAA 1101 AGGAAACCTT CCTTGTGAAG ACCTCAGAGCAT TATATTCCCA GGATGAAAA 1101 AGGAATTTA ATTATGTGA AGAAGATACT TTCTGGATACCA GAATATCAG 1151 TGCATAAGAG ACCACAATAA GAAGAGATACT TTCTGGATCA GGATGAAAA 1201 AAGAGATTTA ATATTGTGA AGAAGATACT TTCTGGATCA GGAATACAGA 1301 ATGGCAAGCA ACCACAATAA GAAGAGATAC TGTCTTATTAT TGCTATGATA 1301 ATGGCAAGCA ACCACAATAA GATGAAGAGA ACAGAAAAGA ACCACAAATAA GATGAAGAGA ACTGTATATAA TTGGGTGGGG 1401 TCTACTTCGG TATATGAGCA ATGAAGAGA ACAGAAAAGA ACACAAAAAG GATAGAAGAAA TTGCTCAAGAA ACACAAAAAA GAACAAAAAAA TTCACCAGAA ACACAAAAAAA GAACAAAAAAA TTCACCAGAA ACACAAAAAAA GAACAAAAAAA TTCACCAGAA AAAAAAAAAA	401	CAGCCAAGAG	TCTGCTTGCC	TGGTTGGACA	GGTCACCATT	TGCTGCTGTG
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601 CTGTCGCAAAC ATTAAACCAA GCGAAGGGCT GGGTAGTATA ATTAAATCTA 701 CATATGATGG CCTCCATGTA ATTAATGGAA 751 GATCGGTCAA AGAAAATCCA TGCTGGCGAT GGGTAGTATA ATTAAATCTA 751 GATCGGTGCA AGAAAATCCA TGCTGGCGAT GAAGTGATTC AAGTTAATCA 801 TCAGACTGTG GTGGGGTGGC AGTTGAAAAA TTTGGTGAAT GCACTACGAG 851 AGGACCCGAG TGGTGGTTATC TTAACTTTAA AAAAGCGACC TCAGAGCATG 901 CTTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA AGCCCCTTGC 951 TCTGCAGCCT CTTATACCTA GAAGTCCCAC AAGCAGCGTT GCCACGCCTT 1001 CCAGCACCAT CAGTACACCC ACCAAAAGA ACCAGTTCTCC GCCCCCCCTTG 1051 CTCTACATTC CCCCTCCTCC TGCAGAACCA TATATTCCCA GGAATCAAT 1101 AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATTATGGTG GGCAGGCCTT 1201 AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATTATGGTG GGCAAGCCAG 1151 TGCATAAGGG ATCTGAATCA CCAAAATCAT TTCTGGATCA GGAATATCGA 1201 AAGAGATTTA ATATTGTCGA AGAAGCACA TATATTGTG GGCAAGCCAG 1301 ATGGCAAGCA ACGACCATA TCTATAGCAG ACGAAATAA TTGGTGAATA 1251 TGAAAAAGGA ACCCTATA TCTATGCCAG TGGAATAATA TTGGTGTGGGG 1351 GACTATGAGA ATCCAAATAA GATCAAGAAG ACCACCAACTT 1401 TCTACCTTGG TATATGAGCA ATGAAAAGA ACGACAAAACT 1401 TCTACTTCGG TATATGAGCA ATGAAAAGA GACACAAGAA AGAACACACT 1401 TCTACCTTGG TATATGAGCA ATGAAAAGA TACTAAAAAAACAT 1551 GGATGCACTG AGACAAAAAG GACACAGGGA AGAACTCAAA 1551 GAATACAAGAA ATTCAAACAA ATGAAAAGAT TCCTCAAGAA AAAAAGAT 1551 GGATGCACTG AGACAAAAAG GACACACGAGA AGAACTCAAA AAAAAAGAT 1551 GAATACAATCA ATTCAAGCAA TCATGGGCC TCCTCAGAAA AAAAAAGAT 1551 GAATACAATCA ATTCAAGCAA TCATGGGCC TCCTGTGCCA GAGACCACC 1601 TATACCATAC ATTCAAGCAG TCCTCACTGC AGCAAATT AAAGAAAAGT 1701 TCTTGGCCGT GGTGACTGT AGGAGACAAAAA AGACGAAAATT CTTGCAAAGA 1701 TCTTGGCCGT GGTGACTGT AGGAGACAAAAAAAAAAA	501	AACAACAATT	GTGCAACAGG	ATTGTACTGT	ATATGAAACA	GAGAATAAAA
651 GCTGGCAAAC ATTAAACCAA GCGAAGGGCT GGGTATGTAT ATTAAATCTA 701 CATATGATGG CCTCCATGTA ATTACTGGAA CCACAGAAAA TTCACCTGCA 751 GATCGGTGCA GGAAAAATCCA TGCTGGCGAT GAAGTGATTC AAGTTAATCA 801 TCAGACTGTG GTGGGGTGC AGTTGAAAAA TTTGGTGAAT GACTTAATCA 801 TCAGACTGTG GTGGGGTGC AGTTGAAAAA TTTGGTGAAT GCACTACGAG 851 AGGACCCGAG TGGTGTTATC TTAACCTTGA AAAAGCGACC TCAGAGCATG 901 CTTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA AGCCCCTTGC 951 TCTGCAGCCT CTTATACCTA GAAGTCCCC AAGCAGCGTT GCCACGGCTT 1001 CCAGCACCAT CAGTACACCC ACCAAAAGAG ACAGTTCTGC CCTCCCAGGAT 1051 CTCTACATTC CCCCTCCTC TGCAGAACCA TATATTCCCA GGGATGAAAA 1101 AGGAAACCTT CCTTGTAAAC ACCACAAAGAG ACAGTTCTGC GGCAAGCACA 1151 TGCATAAGGG ATCTGAATCA CCAAAATCAT TTCTGGATCA GGAATAACA 1201 AAGAGATTTA ATATTCTCGA AGAAGATACT TTCTGGATCA GGCAATGCAT 1301 ATGGCAAGA ACCACAAATAA GTCAAGAGAAACA TATATTCCCA GGAATAACAA 1301 ATGGCAAGCT ACCAAAATAA GTCAAGAAAAAAACTC 1401 TCTACTTCGG TATATGAGCA ATGAAAAAAAAACTC 1401 TCTACTTCGG TATATGAGCA ATGAAAAAAAAAAACTC 1551 GACTATAAAAAAAAAAAAAAAAAAAAAAAACTC 1551 GATAAAAAAAA CAGCAAAAAAA GACAACAAGAAAAAACTC 1710 TCTACACTAC ATTTCAAGCAA TAACACAAGAAAAAAAAAA	551					
701 CATATGATGG CCTCCATGTA ATTACTGGAA CCACAGAAAA TTCACCTGCA 751 GATCGGTGCA AGAAAATCCA TGCTGGCGAT GAGTGATTC AAGTTAATCA 801 TCAGACTGTG GTGGGTGGC AGTTGAAAAA TTTGGTGAAT GCACTACGAG 851 AGGACCGAG TGGTGTTATC TTAACTTTGA AAAAGCGAC TCAGAGGATG 901 CTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA AGCCCTTGC 951 TCTGCAGCCT CTTATACCTCA GAAGACCCA AAGCAGCGTT GCCACGCCTT 1001 CCAGCACCAT CAGTACACCC ACCAAAAGAG ACAGTTCTGC CCTCCAGGAT 1011 AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATATGGTG GGCAGCCAG 1151 TGCATAAGGG ATCTGAATCA CCAAAATCAT TTCTGGATCA GGAATATCAG 1151 TGCATAAGGG ATCTGAATCA CCAAAATCAT TTCTGGATCA GGAATATCAG 1151 TGAAAAAGGA AGATCAGATA ACGACCAGACAG 1151 TGAAAAAGGA ACGACCATAT TCTATGGATCA GGAATATCAG 1151 TGAAAAAGGA AGATCAAGTA GTCTAATTAT GCTATGAATA 1201 AAGGAATTTA ATATTGTCGA AGAAGATACT GTCTTATATT GCTATGAATA 1251 TGAAAAAAGGA ACGACCTATA TCTATGCCAG TGGAATATAA TTGGTGGGG 1351 GACTATGAG ATCCAAATAA GATGAAGAAG ACGAGAAAGC ACCCCAACTT 1301 ATGGCAAAC ACGACCTATA TCTATGCCAG TGGAATATAA TTGGGTGGGG 1451 TCTACTTCGG TATATGAGCA ATGAAAAGAG AGAAGAAAACTC 1401 TCTACTTCGG TATATGAGCA ATGAAAAAGAT TGCTCAAGAA GAATACATGT 1451 TTCAGAGAAA CAGCCAAATAA GATGAAAGAG AGAACTCAAA AAAGAAGGGT 1501 GATAAGAGTA ATAGCCCAAC TCACTATTCA TTGCTACCTA GTTTACAAAT 1501 GAAAAGAGT ATTCAGAGAA TCACTATTCA TTGCTACCTA GTTTACAAAT 1601 TATACCATAC ATTTCAGCAG TCACTATTCA TTGCTACCTA GTTTACAAAT 1601 TATACCATAC ATTTCAGCAG TCACTATTCA TTGCTACCTA GTTTACAAAT 1601 TCTTGGCCGT GGTGACTGTG AGGACAAAAAA AACAAAGGT 1701 TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAA AAAGAAGGAT 1701 TCTTGGCCGT GGTGACTTGT AGGACAAAAAA AACAAAGGAT 1801 GCATCCCTTT ATTGGTAATAT TAATGAGGA GATGAAAAAA AAAGAAGAAT 1801 GCATCCCTTT ATTGGTAATAT TAATGAGGA GATGAAAAAA AAAGAAGAAT 1801 GCATCCCTTT ATTGGTAATAT TAATGAGGA GATGAAAAAA AAAGAAGAT 1801 GCATCCCTTT ATTGGTAATAT TAATGAAGAG AGCCAAATT CATAAGAGAT 1801 GCATCCCTTT ATTGGTAATAT TAATGAAGAG AGCCACAATC AAAGAAAAAA 1801 GAATGCCAC CCCCCAAA TGAAAAAAAA AATGTGTGT CCTAAAAACAA 1801 GAAGGAGAG TCACCAAGGAAAAAAAAAAAAAAAAAAAA	601	CTGTCGTCAG	ATCCTCTGGT	TTCACAGTCT	GCTCACCTGG	AAGTGATTCA
751 GATCGGTGCA AGAAAATCCA TGCTGGCGAT GAAGTGATTC AAGTTAATCA 801 TCAGACTGTG GTGGGGTGGC AGTTGAAAAA TTTGGTGAAT GCACTACGAG 851 AGGACCCGAG TGGTGTTATC TTAACTTTGA AAAAGGGACC TCAGAGCATG 901 CTTACCTCAG CACCAGCTTT ACTGAAAAAA ATGAGATGGA AGCCCCTTGC 951 TCTGCAGCCT CTTATACCTA GAAGTCCAC AAGCAGGGTT GCCACGCCTT 1001 CCAGCACCAT CAGTACACCC ACCAAAGAGA ACAGTTCTGC CCTCCAGGAT 1051 CTCTACATTC CCCCTCCTCC TGCAGAACCA TATATTCCCA GGGATGAAAA 1101 AGGAAACCTT CCTTGTGAGA ACCTCAGAGG ACATTTGGT GCCACGCCTT 1201 AGGAAACCTT CCTTGTGAGA ACCTCAGAGG ACATTTGGT GGCAAGCCAG 1151 TGCATAAAGGG ATCTGAATCA CCAAATCAT TTCTGGATCA GGAATATCGA 1201 AAGAGATTTA ATATTGTCGA AGAAGTACT GTCTTATATT GCTATGAATT 1211 AGGAAAAGGA AGACCTATA TCTATGCCAG TGGAATATCAT 1251 TGAAAAAGGA AGACCTATA TCTATGCCAG TGGAATATAA TTGGGTGGGG 1351 GACTATGAGA ATCCAAATAA GATGAAGAGA GATAGAAGA ACCCCAACTT 1401 TCTACTTCGG TATATGAGCA ATGAAAAGA GAAGAATACA TTGGATGAGA AAAAAACT 1501 GAAAAAGATA ATAGCCCAAC TCACTATCA TTGCTAAGAA GAATACAATA 1501 GAAGAGATA ATAGCCCAAC TCACTATCA TTGCTAAGAA GAAAAACCC 1601 TATACCATCA ATTCCACAC TCACTATCA TTGCTAACATA 1551 GAAGAAGACA ATGAAAAAA GACCAAGAGA AGAAGCCAAAC 1651 AACAAAAGGT CTATAGCAGG CAAGAGAAA AGACCAAATC 1601 TATACCATCA ATTTCAGCAG TCCTCACTGC AGCACAATC CATTACAAT 1701 TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAA AAGAAGAAA 1651 AACAAAAGGTC CTATAGCAGG CAAGAGCAAA AGACCAAATC AAAGAAGAAA 1651 AGCATCCCTTT ATTGGTATGT AGGGGTGGCT TTGGAAAAAA AAAGAAGAAA 1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAA TATTGGTTTGC CCTAAAAGAAA 1801 GCATCCCTTT ATTGGTATT TAATGAGAGG GATGAAAAAC CAGAAGACA 1801 GCATCCCCTTA ATTGGTATAT TAATGAGAGG GATGAAAAAC CAGAAGACA 1801 GCATCCCCTTA ATTGGTATT TAATGAGAGA TTAGACAGAG ATTACTTAGCAGG CAAGAGACAA AGCCAAATC AAAGAAGACA 1801 GCATCCCCTTA ATTGGTATT TAATGAGAGG GATGAAAAAC CAGAAGACA 1801 GCATCCCCTTA ATTGGTATT TAATGAGAG ATTACTTAGCAGG CAAGAAAAAAA TATTGGTTTGT CCTAAAAACATC 1801 GCATGCAGGA TATGCAGAAA AGACAGAAAAAAA TATGGTTTGT CCTAAAAACATAC CCAAAACAAAA	651	GCTGGCAAAC	ATTAAACCAA	GCGAAGGGCT	GGGTATGTAT	ATTAAATCTA
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1101 AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATATGGTG GGCAAGCCAG 1151 TGCATAAGGG ATCTGAATCA CCAAATTCAT TTCTGGATCA GGAATATCGA 1201 AAGAGATTTA ATATTGTCGA AGAAGATACT GTCTTATATT GCTATGAATA 1251 TGAAAAAGGA AGATCAAGTA GTCAAGGAAG ACGCCAACTT 1301 ATGGCAAGCT ACGACCTATA TCTATGCCAG TGGAATATAA TTGGGTGGGG 1351 GACTATGAAG ATCCAAATAA GATGAAGAGA GATGTAAGAA GAGAAAACTC 1401 TCTACTTCGG TATATGAGCA ATGAAAAGAT TGCTCAAGAA GAGAAAACTC 1401 TCTAGAGAAA CAGCAAAAAA GACACAGGGAA AGAAGTCAAA AAAGAAGGT 1501 GATAAGAGTA ATAGCCCAAC TCACTATTCA TTGCTACCTA GTTTACAAAT 1551 GGATGCACTG AGACAAGAAC TCACTATTCA TTGCTACCTA GTTTACAAAT 1551 GGATGCACTG AGACAAGACA TCATGTCATCA TTGCTACCTA GTTTACAAAT 1551 AGACAAAGGTC CTATAGCCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA 1651 AACAAAGGTC CTATAGCCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA 1651 AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAAATT CTTGCAAAGA 1701 TCTTGGCCGT GGTGACTGT AGGGCTGCT TTGGAAAAAG AAAGAAGAAA 1701 TCTTGGCCGT GGTGACTGT AGGACGACAA TTGAAAAAAA ATTGGTTTTT CCTAACGAA 1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGAT 1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 2001 GACTGCAGGA TATGCAGAAA GAAGAGGAAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGAGA GAAGACAAACA ACAAATTACT 2051 GGAGTGAGAG TGACAAGAGA GAAGCAGATA CCCCTCAAC 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAAGCAGATT TCCTCCACGG 2201 GACTGCAGGT CACCCCCATA TGATACATAC CCCACGACCTC CCTCGATGAG 2251 GGAGCAGTG CACTCTAGTCT TCTCATGAGG AGTTTCCCCA GGAAGTAACT 2351 TTCAGACTCT GCCCCTGAGA GACCACTAC CACCACACCCC 2301 CTGGCAGGAT TTAATTGAGA CGCCCCTC CATCCCCAGAC TCCCCCCAGA GAGTTACCTT TCCTCACGG ACAGCATTC CCCCCCAGAC TCCCCCCAGA GAGCAGTA CCCCTTAGC ACGCCCCTC CCTCGAGGT TTAATTGAGA ACCCCTTAGC AAGGTTTACCTT TCCTCCACGG GAGGAGTACC TCCTCTAGAGA ACGCCAGTC CCTTGACCC CATCCCCAGAC TCCCCTGAGA ACGCCAGTC CCTGGAGT TTAATTGAGA ACCCCTTAGC TCCTCTAGACC CCTGGAGT TCCCCTGGAGA ACCCCTCAGA AATGCCAACCACCCC CACCCCATA ACCCATTAGC GAGAGTGAA ACGCCA	1001					
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1501 GATAAGAGTA ATAGCCCAAC TCACTATTCA TTGCTACCTA GTTTACAAAT 1551 GGATGCACTG AGACAAGACA TCATGGGCAC TCCTGTGCCA GAGACCACAC 1601 TATACCATAC ATTTCAGCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA 1651 AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAATTT CTTGCAAAGA 1701 TCTTGGCCGT GGTGACTGT AGGGCTGGCT TTGGAAAAAG AAAGATGCGA 1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAA ATTGGTTTGT CCTAAAGGAT 1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT 1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATC CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 GACTGCAGGA TATGCAGAAA GAGAGGGGG CTTAACCAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTC CATTCGCAAG ACAGCCAGTC AGCGCCCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTTCGCCA GGAAGTAACT 2351 TTCAGACTCT GCCCCTGAG GATTCTGCCA AAGTTCAGCC TCCCCCCGTC 2401 TCCCCCAGAGC ACAGGCGCA GCCCCTC CCTCGATGAC 2451 GCAGGATCAC TATAGGGCCAT ACCCCTTAGC CCAACCCAGA 2551 AGCGGGTCA ACAGGCGGCA GTCTACCCTG CCAACCTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGGCA ACCCCTTAGC CCAACCCAGA 2551 AGCGGGTCA ACCATTGCTG TCTGAATGCT CCAGGTGAG AGGAGGAGGAG AGGAGGAGGAT 2551 AGCGGGTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTCGAGGAT 2551 AGCGGGTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTTGGAGAT 2551 AGCGGGTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGAA GGAAGAGAG GAGGAGGAG GAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG						
1551 GGATGCACTG AGACAAGACA TCATGGGCAC TCCTGTGCCA GAGACCACAC 1601 TATACCATAC ATTTCAGCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA 1651 AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAATTT CTTGCAAAGA 1701 TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAG AAAGATGCGA 1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT 1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT 1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2001 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGGTC TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2351 GGGAGCAGTG CAGTGTCTC CATTCGCAAG ACAGCCCCC AGCCCCCCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGC GGAAGTAACT 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTCAGGC TTACCACTAC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACCCACTC 2451 GCAGGATCAC TATGGGGCCA GCCCCTTAGC CCCACGACCTC 2451 GCAGGATCAC TATGGGGCCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 AGCGGGTTCA ACCACTTGCT TCTCTAGAG GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCACTTGCT TCTGAATGCT CCAGGCGAGC 2501 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAG GAGGAGGAG GAGGAG						
1601 TATACCATAC ATTTCAGCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA 1651 AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAATTT CTTGCAAAGA 1701 TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAG AAAGATGCGA 1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT 1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT 1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACGCCAGTC AGCCCCCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGCCAGTC AGCCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGCCAGTC CCGCGCCTC 231 TTCAGACTCT GCCCTGGAG GATTCTGCCAA ACGCCAGTC CCGCGCCTC 231 TCCCCAGAGC ACAGGCGGC GATTCTGCTA TCTCTGACCC 2401 TCCCCAGAGC ACAGGCGCA GTCTACCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG ACAGGCGGC ATCTCACCTG CCAACTCAGA AATGCCACCT 2451 AGCGGGTTCA ACCATTGCTG TCTGAATGC CCAGGCCATC 2451 AGCGGGTTCA ACCACTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGCC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGGTAGC AGGAAGCAGC 2501 TGCTAAATGG AAATGGGGCC CAGGCGGGG GTTTTACTTT CCTCTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAG						
1651 AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAATTT CTTGCAAAGA 1701 TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAG AAAGATGCGA 1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT 1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT 1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGC GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGCC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGC CCAGTTAGTG CCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGC CCAGTTAGTG CCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTCTGAGAG 2501 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGGAGGAGGAGGAGGAGG						
1701 TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAG AAAGATGCGA 1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT 1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT 1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGAG GAGGAGGAG						
AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT ROLL GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA ASSAC CATTAGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT CACAGACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT CACAGACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT CACAGACAGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA CACAAAACAA CACACACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG CACACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG CACACCCCCATA TCATACAGA AGTTTCGCCA GGAAGTAACT CACACACACCCCCATA TCCATCAGA ACGCCACTT TCCTCCACGG CACACACACAC CCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT CACACACACACACACACACACACACACACACACA				i i	•	
GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT CACCAGACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT CACCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT CACCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT CACCACCATA TGATACATAC CCACGACCTC CCTCGATGAG CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG CACCTCCATCAGC AAGCAAAACA TAGCCGACTT TCCTCACGG CACCCCCATA TCCATCAGA AGTTTCGCCA GGAAGTAACT CACCAGACCTC CACCCCCATA TCCATCAGA ACTCCACCCC GGAAGTAACT CACCAGACCTC CACCCCCATA TCCATCAGA AGTTTCGCCA GGAAGTAACT CACCAGACCTC CATTCGCAAG ACAGCCAGTC AGCCCCCCCCCC						
1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA 1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT 1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT 2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT 2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA TGATACATAC CCACGACCTC CCTCGATGAG TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT GGAGCAGGT CAGTGTCTC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC TCCACGGAGC ACAGGCGGCA GATTCTGTCT TCTCTGACTC CGCGGCCATC CTGCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT CTGCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT CTGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT CTGCTAAATGG AAATGGGGGC CAGGGTGAA GTTTTACTCT GCCTCGAGAT CCCAGAGTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC CAGAGGTTCA ACCATTGCTC TCTGAATGCT CCAGTTAGTG CCTGTGACCC CAGAGGTGGA GAGAGGGAG GAGGAGGAGGAGGAGGAGGAGGAGGA						
GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA 2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG 2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
2151 TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG 2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT 2251 GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC 2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC CAGACTCAGAC CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC CAGACTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC CAGACTCAGACTCA CACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT CAGACTCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG CAGACTCAGA AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT CAGACTCAGA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC CAGAGGTGAA GGAAGAGGAG GAGGAGGAGGAGGAGGAGGAGGAGG						
GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC CTGGCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC CTGCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT CTGCAGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG CTGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT CTGCTAAATGG ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC CTGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA						
2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC 2351 TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC 2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT CASC GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT ACCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT 2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG 2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT 2551 AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT AGCGGGTTCA ACCATTGCTG TCTGAATGCT CCAGTTAGTG CCTGTGACCC ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG						
2551 AGCGGGTTCA ACCATTGCTG TCTGAaTGCT CCAGTTAGTG CCTGTGACCC 2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG		TGCTAAATGG	AAATGGGGGC	AAGCCTCGAA	GTTTTACTCT	GCCTCGAGAT
2651 AGGAGGAAGG GGAGGCAGCA GGGGAAAACA TAGGAGAAAA AAGCTAA	2601	ACAGGATGAC	GTGCAACCCC	CAGAGGTGGA	GGAAGAGGAG	GAGGAGGAGG
	2651	AGGAGGAAGG	GGAGGCAGCA	GGGGAAAACA	TAGGAGAAAA	AAGCTAA

-15/26-Fig. 13: SEQ ID NO. 5: nucleotide sequence of human MAGUIN-1 cDNA

Length: 5749 bp

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1	CGGGCAGCTA	GTCGTGCTCG	GGGCTTCACT	CCCGCGCGTG	AGGCGAGCGG	GCAAGTTGGC
61	TGAGGGCGTG	CGGCAGAGGC	TGCTTCCCTC	GGCGACGCGA	CCCCTCAGCA	ACTCAAGCTA
121	TGAACTGAAG	CTCCCTAGGG	ACGGAGACCG	GAGCGGAGCG	GCGGAGGCAG	CAGCAGCAGC
181	AGCAGCAGCA	GCAGCAGCAG	CAGCCGCCGC	CGCCGCCGCC	TTAGCGGGAA	CTGAGCAGAC
241	CCGGCGCGGA	GCCACGACTC	CTGCACGTTT	ACCTCCCTGT	CGCCGTTCCT	GCCGGCGGTT
301	GGCTAAAAGA	CGTTACAGCC	GCGAGACCCG	ACACACAAAA	GCCGCTTTCT	CCGCGCCGCC
361	CGCCCAGGGA	GGCTGCGGCC	AGCAAGGGAC	CCCACCTGAG	AGCAGCTCGG	GCTGCTGAGT
421	TCGTTTTGTG	TCTGAGCTCT	GCGCTCTGCA	CGGAACCGAC	CCCGTACCCA	TGGCTCTGAT
481	AATGGAACCG	GTGAGCAAAT	GGTCTCCGAG	TCAAGTAGTG	GACTGGATGA	AAGGTCTTGA
541	TGACTGTTTG	CAGCAGTATA	TTAAGAACTT	TGAGAGGGAG	AAGATCAGTG	GGGACCAGCT
601	GCTGCGCATT	ACACATCAGG	AGCTAGAAGA	TCTGGGGGTC	AGCCGCATTG	GCCATCAGGA
661	ACTGATCTTG					
721	TCTAAAAACC	CTTTCTCACA	AGTTGAATGC	ATCTGCCAAA	AATCTGCAGA	ATTTTATAAC
	AGGAAGGAGA					
	TCTGACCTCA					
	GTCACCATTT					
	CCTGGAGTTA					
	TCTTCACGTG					
	TCCTCTGGTT					
1141	CGAAGGGCTG	GGTATGTATA	TTAAATCTAC	ATATGATGGC	CTCCATGTAA	TTACTGGAAC
	CACAGAAAAT					
	AGTTAATCAT					
	GGACCCGAGT					
	ACCAGCTTTA					
	AAGTCCCACA					
	CAGTTCTGCC					
1561	GGATGAAAAA	GGAAACCTTC	CTTGTGAAGA	CCTCAGAGGA	CATATGGTGG	GCAAGCCAGT
	GCATAAGGGA					
1681	TATTGTCGAA	GAAGATACTG	TCTTATATTG	CTATGAATAT	GAAAAAGGAA	GATCAAGTAG
	TCAAGGAAGA					
	GGAATATAAT					
	AGAAAACTCT					
1921	TCAGAGAAAC	AGCAAAAAGG	ACACAGGGAA	GAAGTCAAAA	AAGAAGGGTG	ATAAGAGTAA
1981	TAGCCCAACT	CACTATTCAT	TGCTACCTAG	TTTACAAATG	GATGCACTGA	GACAAGACAT
	CATGGGCACT					
	GCACAAATCA					
	TTGCAAAGAT					
	GAGTTACTTT					
	TTGGTATATT					
2341	AATTGATAGA	GCCAGTGAAT	GCCGCAAAAA	ATATGCATTC	AAAGCCTGTC	ATCCTAAAAT
2401	CAAAAGCTTT	TATTTTGCTG	CTGAACATCT	TGATGATATG	AACAGGTGGC	TTAACAGAAT
	TAATATGCTG					
	GAGTGAGAGT					
	ACCCCCATAT					
	AGCAAAACAT			and the second s		
	GTTTCGCCAG					
	GCGCCGCTCC					
2821	TCAGACTCTG	CCCCTGGAGG	ATTCTGTCTT	CTCTGACTCC	GCGGCCATCT	CCCCAGAGCA

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2881	CAGGCGGCAG	TCTACCCTGC	CAACTCAGAA	ATGCCACCTG	CAGGATCACT	ATGGGCCATA
2941	CCCCTTAGCT	GAGAGTGAGA	GGATGCAAGT	GCTAAATGGA	AATGGGGGCA	AGCCTCGAAG
3001	TTTTACTCTG	CCTCGAGATA	GCGGGTTCAA	CCATTGCTGT	CTGAATGCTC	CAGTTAGTGC
3061	CTGTGACCCA	CAGGATGACG	TGCAACCCCC	AGAGGTGGAG	GAAGAGGAGG	AGGAGGAGGA
3121	GGAGGAAGGG	GAGGCAGCAG	GGGAAAACAT	AGGAGAAAAA	AGTGAAAGCA	GAGAAGAAAA
3181	GTTAGGAGAC	TCATTGCAAG	ATTTATACAG	GGCACTGGAG	CAGGCCAGTC	TGTCACCACT
3241	AGGAGAACAT	CGTATTTCAA	CCAAGATGGA	ATACAAGCTA	TCATTTATAA	AAAGATGTAA
3301	TGATCCTGTA	ATGAATGAAA	AACTACACCG	GCTGAGAATT	CTCAAAAGCA	CTTTAAAGGC
3361	CAGAGAAGGG	GAAGTAGCCA	TTATCGATAA	AGTCCTAGAC	AATCCAGACT	TGACATCTAA
3421	AGAATTCCAA	CAATGGAAGC	AGATGTACCT	CGACCTTTTC	TTGGATATCT	GTCAAAATAC
		GACCCACTGA				
3541	ACACACTCAT	TCATACATTG	AAACGCATGT	CTAAATGTAT	TCTGCCTTCA	GACCATCTAG
3601	TACCTGCTGG	TACTCTGAAC	AAGTATATAA	GGTAGTTTTT	ATATCAATGT	GTGGAACACT
3661	TGACAAGCTA	TACTTTAATG	TTACCAAACT	ATATGAAACA	AACCATATAT	GGTCACAATA
3721	CCACTATCTT	TAATGAGCAT	TTGTATATTT	TATATGCAAC	AGTGCTCAGC	TTATGTTTAC
3781	CATGTGCAAA	ATCAACTGTC	TTTAATGACT	TAAAATTAAC	TTTTGCAAAC	AATTCTAAAT
3841	ACAGGTGGTC	TTCAAGTAGT	AAAACCACAA	AAGGCAGTTT	TCTATCTATG	GTCATCTTTT
3901	CTCCCTTTAA	GTTAATTTTA	TATAAACAAG	ACTTCAAAAG	TAAATCACAT	TTTTTCAGGT
3961	GCAGACATCC	TTGTGGGTGG	GAAAGAATTT	AAACCTTTTT	TATATTTATT	AAAATGTTCT
4021	AAGAATTTTC	TTAAACATTG	CACAAAGTTT	AATGCTGTAG	TTTTATTTTT	GTGAAATGTA
4081	GATGCGCATA	CAAGAGCTAA	GCAAAATAGA	AGAGCATCGA	CATAAGAAAA	GTTCAGGTAT
		TCTTAATAGT				
4201	CAAATCTATG	AGAACACTTG	GTGTATCAGG	GCAAAGCTTT	GTAAGATGTT	TTTGTAACTA
4261	AGACCAAAAT	TGAAGATAGA	GCTGCTTTAT	TTTCTTGGTT	TAAATCTTCC	TTTATTTTTG
4321	TAGTGATGAG	ATGCTGATTG	TGTACAGAAG	AATTTGAGAG	GGGATTTTTA	AAAACTGACT
4381	TAACACACCC	AGAAAGGCAG	CTAACAGCTA	TATATATATA	TAAATTTCAG	CCCAAACTCA
4441	TGTTTTTAAA	CTCCAACTCT	TAAAAGACAA	CAAGGTATAA	ACTGAAATGA	ATCAACTTTC
4501	CACTTAGTTT	CCAATTTTCC	CCTAGTCCAC	TAATTAAACT	TAGGTAATTA	TACTTCAGGT
4561	AGGGAAGTAC	AATATGTTTA	GTTTCAGGCT	GATGTGTGTT	ATAAAAAACA	ACACTGAAAA
4621	ATAAAAATGT	ACTTCCCTTC	TAAGGAGCAA	GCAGGTGATG	GTCATTCAAA	GAGATGTCAC
4681	ATTGAATTAT	GAGAGAAACA	ATTTAGAGGT	TTTTTTCCTG	GCTTCATGAA	TTGTTCTATA
		AGTCTAAGGA				
4801	TTTGAAAGTG	ATCACAGCAT	GAAAATGACT	GTGCTGCTTT	TTAGTGTCTG	GCTGCATAAT
		CAATTTGCTG				
4921	ATATCCTAAA	ATCTACTTCT	AATCAGCTTT	ATACTGTTGC	CTGTACAGCT	CAGTGAATGT
4981	ACTTTCATCT	TTAAGAGTTC	AGATATATGC	CAGTGAATAT	TTTTGCTGTA	GAGGAGAAAG
5041	TAAAAACTCC	ACAGCGGGGA	TCTTTTTCTT	TGCTTTTGAA	ACCACCATTG	AATCACTATC
5101	GTTTTGCAGA	CTTTGCACAA	CTGTACAGGA	GAGTGGCCTT	TCTACAGCAC	ATTTTCAGTA
-		TAGTCAAAAT				
5221	GTCCAGTGTA	ATATTTTTAT	CATTTAAAAA	GAACTCTATT	TGTAAAAACA	TTTATTTACT
5281	GCATGGATAT	TGACGCACAT	TAAATTTGTG	GGATTTTGTA	TATGTAAAAA	AAAAAAAAA
5341	AAAAAAAAAC	AAAAAACCTC	TTGTCCTAAA	ATGAAGTGTG	CTTGTTAACA	GGTGTTTAGA
		TTTACTAGAC				
5461	ATGTGTCATG	TTTACAGTGG	CCAGGTTGTG	GCCTGTAAAC	AGCAAGCAGT	TGACGGGAAG
		TTGCTACTAA				
5581	TGGTAAAAAT	TAAACTAATG	AATTTGACAA	GACTCGTGGC	TAGCCTAGCA	TGAAAGAGAC
		TATATAATAT				TAGGAGAGAG
5701	GCAGCACTGT	AAACTGAAGT	CAAATAAATT	CAGCTCTTAA	TGAATCCTT	

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Fig. 14: SEQ ID NO. 6: nucleotide sequence of human MAGUIN-2 cDNA

Length: 4350 bp

1	GTGCTCGGGG	CTTCACTCCC	GCGCGTGAGG	CGAGCGGGCA	AGTTGGCTGA
51	GGGCGTGCGG	CAGAGGCTGC	TTCCCTCGGC	GACGCGACCC	CTCAGCAACT
101	CAAGCTATGA	ACTGAAGCTC	CCTAGGGACG	GAGACCGGAG	CGGAGCGGCG
151	GAGGCAGCAG	CAGCAGCAGC	AGCAGCAGCA	GCAGCAGCAG	CCGCCGCCGC
201	CGCCGCCTTA	GCGGGAACTG	AGCAGACCCG	GCGCGGAGCC	ACGACTCCTG
251	CACGTTTACC	TCCCTGTCGC	CGTTCCTGCC	GGCGGTTGGC	TAAAAGACGT
301	TACAGCCGCG	AGACCCGACA	CACAAAAGCC	GCTTTCTCCG	CGCCGCCCGC
351	CCAGGGAGGC	TGCGGCCAGC	AAGGGACCCC	ACCTGAGAGC	AGCTCGGGCT
401	GCTGAGTTCG	TTTTGTGTCT	GAGCTCTGCG	CTCTGCACGG	AACCGACCCC
451	GTACCCATGG	CTCTGATAAT	GGAACCGGTG	AGCAAATGGT	CTCCGAGTCA
501	AGTAGTGGAC	TGGATGAAAG	GTCTTGATGA	CTGTTTGCAG	CAGTATATTA
551	AGAACTTTGA	GAGGGAGAAG	ATCAGTGGGG	ACCAGCTGCT	GCGCATTACA
601	CATCAGGAGC	TAGAAGATCT	GGGGGTCAGC	CGCATTGGCC	ATCAGGAACT
651	GATCTTGGAA	GCAGTTGACC	TTCTGTGTGC	ATTGAATTAT	GGCTTGGAAA
701	CAGAAAATCT	AAAAACCCTT	TCTCACAAGT	TGAATGCATC	TGCCAAAAAT
751	CTGCAGAATT	TTATAACAGG	AAGGAGAAGG	AGTGGCCATT	ATGATGGGAG
801	GACCAGCCGA	AAATTGCCAA	ACGACTTTCT	GACCTCAGTT	GTGGATCTGA
851	TTGGAGCAGC	CAAGAGTCTG	CTTGCCTGGT	TGGACAGGTC	ACCATTTGCT
901	GCTGTGACAG	ACTATTCAGT	TACAAGAAAT	AATGTCATAC	AACTCTGCCT
951	GGAGTTAACA	ACAATTGTGC	AACAGGATTG	TACTGTATAT	GAAACAGAGA
1001	ATAAAATTCT	TCACGTGTGT	AAAACTCTTT	CTGGAGTCTG	TGACCACATC
1051	ATATCCCTGT	CGTCAGATCC	TCTGGTTTCA	CAGTCTGCTC	ACCTGGAAGT
1101	GATTCAGCTG	GCAAACATTA	AACCAAGCGA	AGGGCTGGGT	ATGTATATTA
1151	AATCTACATA	TGATGGCCTC	CATGTAATTA	CTGGAACCAC	AGAAAATTCA
1201	CCTGCAGATC	GGTGCAAGAA	AATCCATGCT	GGCGATGAAG	TGATTCAAGT
1251	TAATCATCAG	ACTGTGGTGG	GGTGGCAGTT	GAAAAATTTG	GTGAATGCAC
1301	TACGAGAGGA	CCCGAGTGGT	GTTATCTTAA	CTTTGAAAAA	GCGACCTCAG
1351	AGCATGCTTA	CCTCAGCACC	AGCTTTACTG	AAAAATATGA	GATGGAAGCC
1401	CCTTGCTCTG	CAGCCTCTTA	TACCTAGAAG	TCCCACAAGC	AGCGTTGCCA
1451	CGCCTTCCAG	CACCATCAGT	ACACCCACCA	AAAGAGACAG	TTCTGCCCTC
1501	CAGGATCTCT	ACATTCCCCC	TCCTCCTGCA	GAACCATATA	TTCCCAGGGA
1551	TGAAAAAGGA	AACCTTCCTT	GTGAAGACCT	CAGAGGACAT	ATGGTGGGCA
1601	AGCCAGTGCA	TAAGGGATCT	GAATCACCAA	ATTCATTTCT	GGATCAGGAA
1651	TATCGAAAGA	GATTTAATAT	TGTCGAAGAA	GATACTGTCT	TATATTGCTA
1701	TGAATATGAA	AAAGGAAGAT	CAAGTAGTCA	AGGAAGACGA	GAAAGCACCC
1751	CAACTTATGG	CAAGCTACGA	CCTATATCTA	TGCCAGTGGA	ATATAATTGG
1801	GTGGGGGACT	ATGAAGATCC	AAATAAGATG	AAGAGAGATA	GTAGAAGAGA
1851	AAACTCTCTA	CTTCGGTATA	TGAGCAATGA	AAAGATTGCT	CAAGAAGAAT
1901	ACATGTTTCA	GAGAAACAGC	AAAAAGGACA	CAGGGAAGAA	GTCAAAAAAG
1951	AAGGGTGATA	AGAGTAATAG	CCCAACTCAC	TATTCATTGC	TACCTAGTTT
2001	ACAAATGGAT	GCACTGAGAC	AAGACATCAT	GGGCACTCCT	GTGCCAGAGA
2051	CCACACTATA	CCATACATTT	CAGCAGTCCT	CACTGCAGCA	CAAATCAAAG
2101	AAGAAAAACA	AAGGTCCTAT	AGCAGGCAAG	AGCAAAAGAC	GAATTTCTTG
2151	CAAAGATCTT	GGCCGTGGTG	ACTGTGAGGG	CTGGCTTTGG	AAAAAGAAAG
2201	ATGCGAAGAG	TTACTTTTCA	CAGAAATGGA	AAAAATATTG	GTTTGTCCTA
2251	AAGGATGCAT	CCCTTTATTG	GTATATTAAT	GAGGAGGATG	AAAAAGCAGA

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2301	AGGATTCATT	AGCCTGCCTG	AATTTAAAAT	TGATAGAGCC	AGTGAATGCC
2351	GCAAAAAATA		GCCTGTCATC		
	00				
2401	TTTGCTGCTG	AACATCTTGA	TGATATGAAC	AGGTGGCTTA	ACAGAATTAA
2451	TATGCTGACT	GCAGGATATG	CAGAAAGAGA	GAGGATTAAG	CAGGAACAAG
2501	ATTACTGGAG	TGAGAGTGAC	AAGGAAGAAG	CAGATACTCC	ATCAACACCA
2551	AAACAAGATA	GCCCTCCACC	CCCATATGAT	ACATACCCAC	GACCTCCCTC
2601	GATGAGTTGC	GCCAGTCCTT	ATGTGGAAGC	AAAACATAGC	CGACTTTCCT
2651	CCACGGAGAC	TTCTCAGTCT	CAGTCTTCTC	ATGAGGAGTT	TCGCCAGGAA
2701	GTAACTGGGA	GCAGTGCAGT	GTCTCCCATT	CGCAAGACAG	CCAGTCAGCG
2751	CCGCTCCTGG	CAGGATTTAA	TTGAGACGCC	ACTGACAAGT	TCAGGCTTAC
2801	ACTATCTTCA	GACTCTGCCC	CTGGAGGATT	CTGTCTTCTC	TGACTCCGCG
2851	GCCATCTCCC	CAGAGCACAG	GCGGCAGTCT	ACCCTGCCAA	CTCAGAAATG
2901	CCACCTGCAG	GATCACTATG	GGCCATACCC	CTTAGCTGAG	AGTGAGAGGA
2951	TGCAAGTGCT	AAATGGAAAT	GGGGGCAAGC	CTCGAAGTTT	TACTCTGCCT
3001	CGAGATAGCG	GGTTCAACCA	TTGCTGTCTG	Aatgctccag	TTAGTGCCTG
3051	TGACCCACAG	GATGACGTGC	AACCCCCAGA	GGTGGAGGAA	GAGGAGGAGG
3101	AGGAGGAGGA	GGAAGGGGAG	GCAGCAGGGG	AAAACATAGG	AGAAAAAAGC
3151	TAATACACTG	CGAGAGTTGG	TAGAACCTCT	CCATGCCAAA	TCGGATCCAC
3201	TTCTGTTGGC	ACTCAACCCA	TTGGACTCAC		GCTAATGTTT
3251	AGAGAATTTA	GATCGGAGAG	AGTCGGTACG		AACATCAACC
3301	TCTTGCAAGC	AACTAAAATG	GCCTCGTCCT	TGCTGTTTAT	AACAGAAAAC
3351	AGACTTGTAA	AAAGCTTAGA	TCATCAAGTG	TTTTGGATTG	GGGGCCTCCC
3401	AAAGGGATAT	AAGAGGGGCA	GGCCACTCTT	AAGAAGAATG	CGAGCTTTCT
3451	ACATTGGGAC	TAGCATAAGA	TCAAAGCCAA	TCAAGATGGA	GCACAGTAAC
3501	AGAAAACTGC		GGAGAACAGA	AGGGGAAAGG	GTCTTAACTG
3551	GGAAAGGGCT		ACACCTCAGT	TGTGTTCTCC	TGACACCAGG
3601	AAAAGAGAGG	GATCAGCTTC	AATAACTAGA	AAATTCTGGC	TGTTTAATGG
3651	ACTCTTTGGT	GGCCTCTTTA	AGGCAAAGCA	GAGAAAGCAA	ATTATGTATT
3701	AAGTGTATTT		AAACTTGACG	TGCTGTATTG	TACTAAATTA
3751	AGTGTAATCT	ATTAAGGCAA	GGTATACACA	ATTTGCTTTG	AAACTTACTA
3801	TGTTTATTCT	ATTATAAAGT	GTATTCAGGT	GCAACACAGA	GACTGCTTTC
3851		ATGAAGAAAA	TTTCTCATGC	CAGGCTTTAT	TATAGAATCT
3901	TCAGCTAAAA	TCCTAACTTT	CTCCTTATTT	CTTGGCACTT	GTATACAAGT
3951	GGTGTTGCCT	CTTAGGGCAG	GCATGAGCTA	TTCTTTTCTG	TAAAATATTT
4001		GGCTGTGGGT	TTCATTTTTG	AAAAGTATTT	TGTCTGGATG
4051	TCTTTCAAAC	TAGCTTCAGA	TATTATTTAA	TACTATGTAA	CTGGGTCCCC
4101	TATGGCTCAA	TCAATATTGC	TTATTTTTCT	TCTGTAGTGG	ATGTGAAATT
4151	TCCTTTAGTT	GGATAAGATA	CACTGTAATA	ATTTTAATGC	TAATTAATGA
4201	TATTTCATAC	TGTGCAATGA	ACAGATAATT	TAACACTGTA	TTTTGAAATG
4251	TTTTTTTTTT	CCTGTCACCG	CAGTGTGTGG	TATTGCATAA	TGTGAATACC
4301	TGTAAAAATA	TAAATTACTT	AAAAATAAAA	ATATGACCAA	TTGGTATCAG

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Figure 15: SEQ ID NO. 7

Length: 50 bp

1 GGAGAGAGCACCACTGTAAACTGAAGTCAAATAAATTCAGCTCTTAATG

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Fig. 16: Alignment of SEQ ID NO. 7 with human MAGUIN-1 cDNA

Length: 50 bp

Fig. 17: Schematic alignment of SEQ ID NO. 5, SEQ ID NO. 6 and SEQ ID NO. 7 with Genome Database EST-cluster

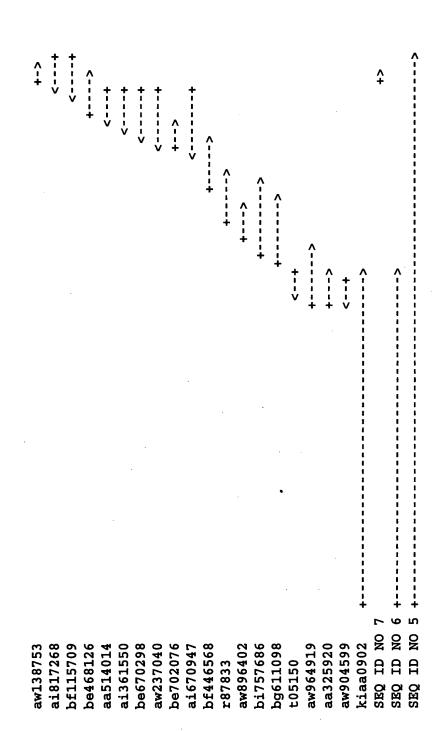


Fig. 18: Images of the human cerebral cortex labeled with anti-Maguin-1 antiserum **_** and with DAPI Ø

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Table 1:

sample	Δ (fold) (frontal / temporal cortex)	
patient P0	12 2.46	
patient P0		
patient P0	1.68	
control C0	11 1.28	
control C0	12 1.29	
control C0	14 0.30	
control C0	05 1.36	
control C0	08 1.15	

Table 2:

sample (front	Δ (fold) al cortex / hippocampus)
patient P012	1.37
patient P016	3.07
patient P010	2.99
patient P011	2.28
patient P014	1.21
patient P019	1.48
control C005	1.74
control C008	0.39
control C004	0.87

Table 3:

sample (fr	Δ (fold) (frontal / temporal cortex)	
patient P012	2.68	
patient P016	2.72	
patient P010	11.73	
patient P011	2.44	
patient P014	1.77	
patient P017	3.43	
patient P019	4.02	
control C011	1.42	
control C012	1.22	
control C014	0.30	
control C005	0.92	
control C008	0.81	

Table 4:

sample	Δ (fold)
	(frontal cortex / hippocampus)

patient P012	1.57
patient P016	4.38
patient P010	9.08
patient P011	4.53
patient P014	0.72
patient P019	1.37
control C005	1.84
control C008	0.46
control C004	1.69

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